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RAW SEQUENCE LISTING

DATE: 01/22/2002

PATENT APPLICATION: US/10/037,270

TIME: 14:28:38

Input Set : D:\pt_FL.784CIP2B.071000.fix

Output Set: N:\CRF3\01182002\J037270.raw

ENTERED

PS

4 <110> APPLICANT: Tang, Y. Tom
 5 Liu, Chenghua
 6 Asundi, Vinod
 7 Zhang, Jie
 8 Ren, Feiyan
 9 Chen, Rui-hong
 10 Zhao, Qing A.
 11 Wehrman, Tom
 12 Xue, Aidong J.
 13 Yang, Yonghong
 14 Wang, Jian-Rui
 15 Zhou, Ping
 16 Ma, Yunqing
 17 Wang, Dunrui
 18 Wang, Zhiwei
 19 Tillinghast, John
 20 Drmanac, Radoje T.
 23 <120> TITLE OF INVENTION: Novel Nucleic Acids and
 24 Polypeptides
 28 <130> FILE REFERENCE: 784CIP2B
 C--> 30 <140> CURRENT APPLICATION NUMBER: US/10/037,270
 C--> 31 <141> CURRENT FILING DATE: 2002-01-04
 33 <150> PRIOR APPLICATION NUMBER: 09/552,317
 34 <151> PRIOR FILING DATE: 2000-04-25
 36 <150> PRIOR APPLICATION NUMBER: 09/488,725
 37 <151> PRIOR FILING DATE: 2000-01-21
 40 <160> NUMBER OF SEQ ID NOS: 1104
 42 <170> SOFTWARE: pt_FL_genes Version 1.0
 48 <210> SEQ ID NO: 1
 49 <211> LENGTH: 2063
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Homo sapiens
 53 <220> FEATURE:
 54 <221> NAME/KEY: CDS
 55 <222> LOCATION: (1)..(1677)
 57 <400> SEQUENCE: 1
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 59 Met Arg Phe Ser Leu Asp Lys Asp Thr Gly Leu Ile Met Leu Ile Ala
 60 1 5 10 15
 62 agg ctg gac tat gag ctc atc cag cgc ttc acc ctg acg atc att gcc 96
 63 Arg Leu Asp Tyr Glu Leu Ile Gln Arg Phe Thr Leu Thr Ile Ile Ala
 64 20 25 30
 66 cgg gac ggg ggc ggc gag gag acc aca ggc cgg gtc agg atc aat gtg 144

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67 Arg Asp Gly Gly Gly Glu Glu Thr Thr Gly Arg Val Arg Ile Asn Val
68          35          40          45
70 ttg gat gtc aac gac aac gtg ccc acc ttc cag aag gat gcc tac gtg      192
71 Leu Asp Val Asn Asp Asn Val Pro Thr Phe Gln Lys Asp Ala Tyr Val
72          50          55          60
74 ggt gct ctg cgg gag aac gag cct tct gtc aca cag ctg gtg cgg ctc      240
75 Gly Ala Leu Arg Glu Asn Glu Pro Ser Val Thr Gln Leu Val Arg Leu
76          65          70          75          80
78 cgg gca aca gat gaa gac tcc cct ccc aac aac cag atc acc tac agc      288
79 Arg Ala Thr Asp Glu Asp Ser Pro Pro Asn Asn Gln Ile Thr Tyr Ser
80          85          90          95
82 att gtc agt gca tct gcc ttt ggc agc tac ttc gac atc agc ctg tac      336
83 Ile Val Ser Ala Ser Ala Phe Gly Ser Tyr Phe Asp Ile Ser Leu Tyr
84          100          105          110
86 gag ggc tat gga gtg atc agc gtc agt cgc ccc ctg gat tat gaa cag      384
87 Glu Gly Tyr Gly Val Ile Ser Val Ser Arg Pro Leu Asp Tyr Glu Gln
88          115          120          125
90 ata tcc aat ggg ctg att tat ctg acg gtc atg gcc atg gat gct ggc      432
91 Ile Ser Asn Gly Leu Ile Tyr Leu Thr Val Met Ala Met Asp Ala Gly
92          130          135          140
94 aac ccc cct ctc aac agc acc gtc cct gtc acc atc gag gtg ttt gat      480
95 Asn Pro Pro Leu Asn Ser Thr Val Pro Val Thr Ile Glu Val Phe Asp
96          145          150          155          160
98 gag aat gac gac cct ccc acc ttc agc aag ccc gcc tac ttc gtc tcc      528
99 Glu Asn Asp Asp Pro Pro Thr Phe Ser Lys Pro Ala Tyr Phe Val Ser
100          165          170          175
102 gtg gtg gag aac atc atg gca gga gcc acg gtg ctg ttc ctg aat gcc      576
103 Val Val Glu Asn Ile Met Ala Gly Ala Thr Val Leu Phe Leu Asn Ala
104          180          185          190
106 aca gac ctg gac cgc tcc cgg gag tac ggc cag gag tcc atc atc tac      624
107 Thr Asp Leu Asp Arg Ser Arg Glu Tyr Gly Gln Glu Ser Ile Ile Tyr
108          195          200          205
110 tcc ttg gaa ggc tcc acc cag ttt cgg atc aat gcc cgc tca ggg gaa      672
111 Ser Leu Glu Gly Ser Thr Gln Phe Arg Ile Asn Ala Arg Ser Gly Glu
112          210          215          220
114 atc acc acc acg tct ctg ctt gac cga gag acc aag tct gaa tac atc      720
115 Ile Thr Thr Thr Ser Leu Leu Asp Arg Glu Thr Lys Ser Glu Tyr Ile
116          225          230          235          240
118 ctc atc gtt cgc gca gtg gac ggg ggt gtg ggc cac aac cag aaa act      768
119 Leu Ile Val Arg Ala Val Asp Gly Gly Val Gly His Asn Gln Lys Thr
120          245          250          255
122 ggc atc gcc acc gta aac atc acc ctc ctg gac atc aac gac aac cac      816
123 Gly Ile Ala Thr Val Asn Ile Thr Leu Leu Asp Ile Asn Asp Asn His
124          260          265          270
126 ccc acg tgg aag gac gca ccc tac tac atc aac ctg gtg gag atg acc      864
127 Pro Thr Trp Lys Asp Ala Pro Tyr Tyr Ile Asn Leu Val Glu Met Thr
128          275          280          285
130 cct cca gac tct gac gtg acc acg gtg gtg gct gtt gac cca gac ctg      912
131 Pro Pro Asp Ser Asp Val Thr Thr Val Val Ala Val Asp Pro Asp Leu

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|-----|---|------|-----|--|
| 132 | 290 | 295 | 300 | |
| 134 | ggg gag aat ggc acc ctg gtg tac agc atc cag cca ccc aac aag ttc | 960 | | |
| 135 | Gly Glu Asn Gly Thr Leu Val Tyr Ser Ile Gln Pro Pro Asn Lys Phe | | | |
| 136 | 305 310 315 320 | | | |
| 138 | tac agc ctc aac agc acc acg ggc aag atc cgc acc acc cac gcc atg | 1008 | | |
| 139 | Tyr Ser Leu Asn Ser Thr Thr Gly Lys Ile Arg Thr Thr His Ala Met | | | |
| 140 | 325 330 335 | | | |
| 142 | ctg gac cgg gag aac ccc gac ccc cat gag gcc gag ctg atg cgc aaa | 1056 | | |
| 143 | Leu Asp Arg Glu Asn Pro Asp Pro His Glu Ala Glu Leu Met Arg Lys | | | |
| 144 | 340 345 350 | | | |
| 146 | atc gtc gtc tct gtt act gac tgt ggc agg ccc cct ctg aaa gcc acc | 1104 | | |
| 147 | Ile Val Val Ser Val Thr Asp Cys Gly Arg Pro Pro Leu Lys Ala Thr | | | |
| 148 | 355 360 365 | | | |
| 150 | agc agt gcc aca gtg ttt gtg aac ctc ttg gat ctc aat gac aat gac | 1152 | | |
| 151 | Ser Ser Ala Thr Val Phe Val Asn Leu Leu Asp Leu Asn Asp Asn Asp | | | |
| 152 | 370 375 380 | | | |
| 154 | ccc acc ttt cag aac ctg cct ttt gtg gcc gag gtg ctt gaa ggc atc | 1200 | | |
| 155 | Pro Thr Phe Gln Asn Leu Pro Phe Val Ala Glu Val Leu Glu Gly Ile | | | |
| 156 | 385 390 395 400 | | | |
| 158 | ccg gcg ggg gtc tcc atc tac caa gtg gtg gcc atc gac ctc gat gag | 1248 | | |
| 159 | Pro Ala Gly Val Ser Ile Tyr Gln Val Val Ala Ile Asp Leu Asp Glu | | | |
| 160 | 405 410 415 | | | |
| 162 | ggc ctg aac ggc ctg gtg tcc tac cgc atg ccg gtg ggc atg ccc cgc | 1296 | | |
| 163 | Gly Leu Asn Gly Leu Val Ser Tyr Arg Met Pro Val Gly Met Pro Arg | | | |
| 164 | 420 425 430 | | | |
| 166 | atg gac ttc ctc atc aac agc agc agc ggc gtg gtg gtc acc acc acc | 1344 | | |
| 167 | Met Asp Phe Leu Ile Asn Ser Ser Ser Gly Val Val Val Thr Thr Thr | | | |
| 168 | 435 440 445 | | | |
| 170 | gag ctg gac cgc gag cgc atc gcg gag tac cag ctg cgg gtg gtg gcc | 1392 | | |
| 171 | Glu Leu Asp Arg Glu Arg Ile Ala Glu Tyr Gln Leu Arg Val Val Ala | | | |
| 172 | 450 455 460 | | | |
| 174 | agt gat gca ggc acg ccc acc aag agc tcc acc agc acg ctc acc atc | 1440 | | |
| 175 | Ser Asp Ala Gly Thr Pro Thr Lys Ser Ser Thr Ser Thr Leu Thr Ile | | | |
| 176 | 465 470 475 480 | | | |
| 178 | cat gtg ctg gat gtg aac gac gag acg ccc acc ttc ttc ccg gcc gtg | 1488 | | |
| 179 | His Val Leu Asp Val Asn Asp Glu Thr Pro Thr Phe Phe Pro Ala Val | | | |
| 180 | 485 490 495 | | | |
| 182 | tac aat gtg tct gtg tcc gag gac gtg cca cgc gag ttc cgg gtg gtc | 1536 | | |
| 183 | Tyr Asn Val Ser Val Ser Glu Asp Val Pro Arg Glu Phe Arg Val Val | | | |
| 184 | 500 505 510 | | | |
| 186 | tgg ctg aac tgc acg gac aac gac gtg ggc ctc aat gca gag ctc agc | 1584 | | |
| 187 | Trp Leu Asn Cys Thr Asp Asn Asp Val Gly Leu Asn Ala Glu Leu Ser | | | |
| 188 | 515 520 525 | | | |
| 190 | tac ttc atc aca ggt gct gcc ccg gcc tcc acc cac ctg tgc agg cct | 1632 | | |
| 191 | Tyr Phe Ile Thr Gly Ala Ala Pro Ala Ser Thr His Leu Cys Arg Pro | | | |
| 192 | 530 535 540 | | | |
| 194 | cct ggg gcc ctg cct cca ccc ctc cca gat gga cag cca gac tag gtg | 1680 | | |
| 195 | Pro Gly Ala Leu Pro Pro Pro Leu Pro Asp Gly Gln Pro Asp | | | |
| 196 | 545 550 555 | | | |

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198  ggggcaggtg aggggtgaaa agaggtcagg gctctactgt tgggctttag cctctggtgg 1740
200  tgcctcccga ggatttgctc ctggctcttc ccaagggcct tgcagctgga tcaactctgga 1800
202  ctggctccct ggggacctcc tgaacctgtt ggttgaggg acggggagca tctaccaagg 1860
204  ttcattctag agggaggtaa ggcccctatga ttcctaggga ggagccctga gcccactcc 1920
206  ccgcccgaag tctgggtgac agagcagtga cttggaggaa tgtggcctca tccttccttg 1980
208  gggacctgtt gagaattccc acctgttttag aggcagatgg ttttgatctc cctaaatgaa 2040
210  atggttttag ctcaaaaaaa aaa 2063
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216 <211> LENGTH: 1352
217 <212> TYPE: DNA
218 <213> ORGANISM: Homo sapiens
220 <220> FEATURE:
221 <221> NAME/KEY: CDS
222 <222> LOCATION: (209)..(673)
224 <400> SEQUENCE: 2
225  acaaccgttg cttttttaag agaggcccgg cccatccaga ggggggtgggg cagaggcgga 60
227  gtctgaggag ctggggaagg aacaaagcga ggctgcggg cggcggctgg gctccggcgg 120
229  ggccgcgggg tgcggggcct gcgggcggcg gcccgggcgg agcgttgagg ggaaggaggt 180
231  ggcacgcgcg tccgcgcgg ccccggcc atg aac ggg ctc ccc tcg gca gag 232
232                                     Met Asn Gly Leu Pro Ser Ala Glu
233                                     1 5
235  gcg ccg ggc ggg gcg ggc tgc gct ttg gcc ggg ctc cca ccg ctg ccg 280
236  Ala Pro Gly Gly Ala Gly Cys Ala Leu Ala Gly Leu Pro Pro Leu Pro
237  10 15 20
239  cgc ggc ctc agc ggc ctc ctt aat gcg agc ggg ggc tcg tgg cgg gag 328
240  Arg Gly Leu Ser Gly Leu Leu Asn Ala Ser Gly Gly Ser Trp Arg Glu
241  25 30 35 40
243  ctg gag cgc gtc tac agc cag cgc agc cgc atc cac gac gag ctg agc 376
244  Leu Glu Arg Val Tyr Ser Gln Arg Ser Arg Ile His Asp Glu Leu Ser
245  45 50 55
247  cgc gcc gcc cgc gcc ccg gac ggg ccc cgc cac gcc gcc ggc gcc gcc 424
248  Arg Ala Ala Arg Ala Pro Asp Gly Pro Arg His Ala Ala Gly Ala Ala
249  60 65 70
251  aac gcg gga ccc gca gcc ggc ccg cgt cgt cct gtc aac ctc gac tca 472
252  Asn Ala Gly Pro Ala Ala Gly Pro Arg Arg Pro Val Asn Leu Asp Ser
253  75 80 85
255  gcg ctg gcc gcg ctg cgc aag gag atg ttg tct gca ggt ggg gct gcg 520
256  Ala Leu Ala Ala Leu Arg Lys Glu Met Leu Ser Ala Gly Gly Ala Ala
257  90 95 100
259  gca gtt gga cat gtc ctt gtt gtg cca gct gtg ggg cct gta cga gtc 568
260  Ala Val Gly His Val Leu Val Val Pro Ala Val Gly Pro Val Arg Val
261  105 110 115 120
263  aat cca gga cta caa aca cct gtg cca aga cct gag ctt ctg cca gga 616
264  Asn Pro Gly Leu Gln Thr Pro Val Pro Arg Pro Glu Leu Leu Pro Gly
265  125 130 135
267  cct gtc atc ctc cct cca ttc gga cag ctc cta ccc acc gga tgc ggg 664
268  Pro Val Ile Leu Pro Pro Phe Gly Gln Leu Leu Pro Thr Gly Cys Gly
269  140 145 150
271  cct gtc tga cgacgag gagcctcccg atgccagcct gcctcctgac ccgccacccc 720

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272 Pro Val
275 ttactgtgcc ccagacgcac aatgcccgtg accagtggct gcaggatgcc ttccacatca 780
277 gcctctgaag ggctgggggg cagggggcat gcacccatgc aaaaggctca gaaactcccc 840
279 ctccggcaag ccctcagact tcggagcctg cgccttcccc cctaccgcct cacctcacag 900
281 gagggccagg catgtattcc tcagaggcga aactgccaaa ctctttctcc tgtcttgggt 960
283 tggctggcac tggggcgggc atctagggta cagcctctgc tcatggcact gggcctccag 1020
285 ttcttccaca tgtgtgcacc ccagcttggt ccaaccctca gccttgcggt ggggcccga 1080
287 gcatcttccc ttccgcttgg cgtctctggg attgggatga gtgcctggct cccatctcct 1140
289 cctcaccttt tgttgcatac ggcagctgct ggctcagggg catccacct ccgggctctg 1200
291 ggttctctcg ccctggaagg gctccaggac ccgtcccaat aaccacccac ggccaggagg 1260
293 gccaaaggcc cgtgctggat atttaaattt aggggcccgt ctccaggggcg cgtagataaa 1320
295 taaatacact cagcgtcaaa aaaaaaaaaa aa 1352
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301 <211> LENGTH: 5143
302 <212> TYPE: DNA
303 <213> ORGANISM: Homo sapiens
305 <220> FEATURE:
306 <221> NAME/KEY: CDS
307 <222> LOCATION: (501)..(4277)
309 <400> SEQUENCE: 3
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312 aaaaagagat ctctcgagga tccgaattcg cggccgcgtc gaccgcgccc ctgccgcggc 120
314 ccctagctcg ggccctcagg gcctcccctt tccgggcagg ccggtcccgt cagcaaggca 180
316 gtgagcaccg cggccagcag agggcggtcc ggacccaagt ctgcagcggc gccattggcg 240
318 tgtggaaaat gccaccagat ggcgggttag gattgcagct ccgttggaagg cgcggccccc 300
320 gctcccgaac ccccggcgac caccctgtaa caaccccccc acatcgggaa taacacaccg 360
322 gagacttttg gggggaaact aggtcgatgg tcggcggcgc ccggatgggc agctgaggat 420
324 tgccttttag gttattttta aagtttttag ttgtacagca cttgattatt ttgctgcatt 480
326 gtgaaaggac ctctccagca atg att act tca gaa tta cca gtg tta cag 530
327 Met Ile Thr Ser Glu Leu Pro Val Leu Gln
328 1 5 10
330 gat tca act aat gaa act act gcc cat tcc gat gct ggc agc gag ctt 578
331 Asp Ser Thr Asn Glu Thr Thr Ala His Ser Asp Ala Gly Ser Glu Leu
332 15 20 25
334 gaa gaa aca gag gtc aaa gga aaa aga aaa agg ggt cgt cct ggc cgg 626
335 Glu Glu Thr Glu Val Lys Gly Lys Arg Lys Arg Gly Arg Pro Gly Arg
336 30 35 40
338 cct cca tct aca aat aag aaa cct cga aaa tct cca ggt gag aag agc 674
339 Pro Pro Ser Thr Asn Lys Lys Pro Arg Lys Ser Pro Gly Glu Lys Ser
340 45 50 55
342 aga att gaa gct gga att aga gga gca ggc cgt gga aga gct aat gga 722
343 Arg Ile Glu Ala Gly Ile Arg Gly Ala Gly Arg Gly Arg Ala Asn Gly
344 60 65 70
346 cac cct caa cag aat ggg gaa ggg gag cct gtc aca tta ttt gag gtg 770
347 His Pro Gln Gln Asn Gly Glu Gly Glu Pro Val Thr Leu Phe Glu Val
348 75 80 85
350 gtg aaa ctg ggg aaa agt gca atg cag tcc gtg gtg gat gac tgg att 818
351 Val Lys Leu Gly Lys Ser Ala Met Gln Ser Val Val Asp Asp Trp Ile
352 95 100 105

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→ Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : D:\pt_FL.784CIP2B.071000.fix

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L:30 M:270 C: Current Application Number differs, Replaced Current Application Number
L:31 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:2008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:2012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:2206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:7920 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:8681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:8845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:11343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
L:11717 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:11719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:11721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:12082 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:12979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:21539 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110
L:21541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110
L:29074 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:144
L:31963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:156
L:31967 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:156
L:31969 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:156
L:33650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:165
L:35021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:36554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:37368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:188
L:37428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:188
L:37430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:188
L:37432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:188
L:40315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206
L:40411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206
L:40413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206
L:46364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:242
L:52411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:263
L:54132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:270
L:55761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:279
L:58873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:293
L:59157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:294
L:59511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:295
L:59513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:295
L:61314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:303
L:67002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:330
L:67004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:330
L:68053 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:332
L:74607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:356
L:74609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:356

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L:74833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:357
L:74835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:357
L:74855 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:358
L:76524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:367